

SEQUENCE LISTING

COPY

(1) GENERAL INFORMATION:

- (i) APPLICANT: CRAIG, NANCY L
- (ii) TITLE OF INVENTION: GAIN OF FUNCTION MUTATIONS IN
ATP-DEPENDENT TRANSPOSITION PROTEINS
- (iii) NUMBER OF SEQUENCES: 15
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Anne Brown (Alston & Bird, LLP)
 - (B) STREET: 3605 Glenwood Ave.
 - (C) CITY: Raleigh
 - (D) STATE: NC
 - (E) COUNTRY: USA
 - (F) ZIP: 27608
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Brown, Anne
 - (B) REGISTRATION NUMBER: 36,463
 - (C) REFERENCE/DOCKET NUMBER: 5789-3
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 919 420 2205
 - (B) TELEFAX: 919 881 3175

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1670 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..1668

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG AGT GCT ACC CGG ATT CAA GCA GTT TAT CGT GAT ACG GGG GTA GAG	48
Met Ser Ala Thr Arg Ile Gln Ala Val Tyr Arg Asp Thr Gly Val Glu	
1 5 10 15	
GCT TAT CGT GAT AAT CCT TTT ATC GAG GCC TTA CCA CCA TTA CAA GAG	96
Ala Tyr Arg Asp Asn Pro Phe Ile Glu Ala Leu Pro Pro Leu Gln Glu	
20 25 30	
TCA GTG AAT AGT GCT GCA TCA CTG AAA TCC TCT TTA CAG CTT ACT TCC	144
Ser Val Asn Ser Ala Ala Ser Leu Lys Ser Ser Leu Gln Leu Thr Ser	
35 40 45	
TCT GAC TTG CAA AAG TCC CGT GTT ATC AGA GCT CAT ACC ATT TGT CGT	192
Ser Asp Leu Gln Lys Ser Arg Val Ile Arg Ala His Thr Ile Cys Arg	
50 55 60	
ATT CCA GAT GAC TAT TTT CAG CCA TTA GGT ACG CAT TTG CTA CTA AGT	240
Ile Pro Asp Asp Tyr Phe Gln Pro Leu Gly Thr His Leu Leu Leu Ser	
65 70 75 80	
GAG CGT ATT TCG GTC ATG ATT CGA GGT GGC TAC GTA GGC AGA AAT CCT	288
Glu Arg Ile Ser Val Met Ile Arg Gly Gly Tyr Val Gly Arg Asn Pro	
85 90 95	
AAA ACA GGA GAT TTA CAA AAG CAT TTA CAA AAT GGT TAT GAG CGT GTT	336
Lys Thr Gly Asp Leu Gln Lys His Leu Gln Asn Gly Tyr Glu Arg Val	
100 105 110	
CAA ACG GGA GAG TTG GAG ACA TTT CGC TTT GAG GAG GCA CGA TCT ACG	384
Gln Thr Gly Glu Leu Glu Thr Phe Arg Phe Glu Glu Ala Arg Ser Thr	
115 120 125	
GCA CAA AGC TTA TTG TTA ATT GGT TGT TCT GGT AGT GGG AAG ACG ACC	432
Ala Gln Ser Leu Leu Leu Ile Gly Cys Ser Gly Ser Gly Lys Thr Thr	
130 135 140	
TCT CTT CAT CGT ATT CTA GCC ACG TAT CCT CAG GTG ATT TAC CAT CGT	480
Ser Leu His Arg Ile Leu Ala Thr Tyr Pro Gln Val Ile Tyr His Arg	
145 150 155 160	
GAA CTC AAT GTA GAG CAG GTG GTG TAT TTG AAA ATA GAC TGC TCG CAT	528
Glu Leu Asn Val Glu Gln Val Val Tyr Leu Lys Ile Asp Cys Ser His	
165 170 175	
AAT GGT TCG CTA AAA GAA ATC TGC TTG AAT TTT TTC AGA GCG TTG GAT	576
Asn Gly Ser Leu Lys Glu Ile Cys Leu Asn Phe Phe Arg Ala Leu Asp	
180 185 190	
CGA GCC TTG GGC TCG AAC TAT GAG CGT CGT TAT GGC TTA AAA CGT CAT	624
Arg Ala Leu Gly Ser Asn Tyr Glu Arg Arg Tyr Gly Leu Lys Arg His	
195 200 205	
GGT ATA GAA ACC ATG TTG GCT TTG ATG TCG CAA ATA GCC AAT GCA CAT	672
Gly Ile Glu Thr Met Leu Ala Leu Met Ser Gln Ile Ala Asn Ala His	
210 215 220	
GCT TTA GGG TTG TTG GTT ATT GAT GAA ATT CAG CAT TTA AGC CGC TCT	720

Ala	Leu	Gly	Leu	Leu	Val	Ile	Asp	Glu	Ile	Gln	His	Leu	Ser	Arg	Ser		
225					230					235					240		
CGT	TCG	GGT	GGA	TCT	CAA	GAG	ATG	CTG	AAC	TTT	TTT	GTG	ACG	ATG	GTG		768
Arg	Ser	Gly	Gly	Ser	Gln	Glu	Met	Leu	Asn	Phe	Phe	Val	Thr	Met	Val		
				245					250					255			
AAT	ATT	ATT	GGC	GTA	CCA	GTG	ATG	TTG	ATT	GGT	ACC	CCT	AAA	GCA	CGA		816
Asn	Ile	Ile	Gly	Val	Pro	Val	Met	Leu	Ile	Gly	Thr	Pro	Lys	Ala	Arg		
			260					265					270				
GAG	ATT	TTT	GAG	GCT	GAT	TTG	CGG	TCT	GCA	CGT	AGA	GGG	GCA	GGG	TTT		864
Glu	Ile	Phe	Glu	Ala	Asp	Leu	Arg	Ser	Ala	Arg	Arg	Gly	Ala	Gly	Phe		
		275					280					285					
GGA	GCT	ATA	TTC	TGG	GAT	CCT	ATA	CAA	CAA	ACG	CAA	CGT	GGA	AAG	CCC		912
Gly	Ala	Ile	Phe	Trp	Asp	Pro	Ile	Gln	Gln	Thr	Gln	Arg	Gly	Lys	Pro		
		290				295					300						
AAT	CAA	GAG	TGG	ATC	GCT	TTT	ACG	GAT	AAT	CTT	TGG	CAA	TTA	CAG	CTT		960
Asn	Gln	Glu	Trp	Ile	Ala	Phe	Thr	Asp	Asn	Leu	Trp	Gln	Leu	Gln	Leu		
305					310					315					320		
TTA	CAA	CGC	AAA	GAT	GCG	CTG	TTA	TCG	GAT	GAG	GTC	CGT	GAT	GTG	TGG		1008
Leu	Gln	Arg	Lys	Asp	Ala	Leu	Leu	Ser	Asp	Glu	Val	Arg	Asp	Val	Trp		
				325					330					335			
TAT	GAG	CTA	AGC	CAA	GGA	GTG	ATG	GAC	ATT	GTA	GTA	AAA	CTT	TTT	GTA		1056
Tyr	Glu	Leu	Ser	Gln	Gly	Val	Met	Asp	Ile	Val	Val	Lys	Leu	Phe	Val		
			340					345					350				
CTC	GCT	CAG	CTC	CGT	GCG	CTA	GCT	TTA	GGC	AAT	GAG	CGT	ATT	ACC	GCT		1104
Leu	Ala	Gln	Leu	Arg	Ala	Leu	Ala	Leu	Gly	Asn	Glu	Arg	Ile	Thr	Ala		
		355					360					365					
GGT	TTA	TTG	CGG	CAA	GTG	TAT	CAA	GAT	GAG	TTA	AAG	CCT	GTG	CAC	CCC		1152
Gly	Leu	Leu	Arg	Gln	Val	Tyr	Gln	Asp	Glu	Leu	Lys	Pro	Val	His	Pro		
	370					375					380						
ATG	CTA	GAG	GCA	TTA	CGC	TCG	GGT	ATC	CCA	GAA	CGC	ATT	GCT	CGT	TAT		1200
Met	Leu	Glu	Ala	Leu	Arg	Ser	Gly	Ile	Pro	Glu	Arg	Ile	Ala	Arg	Tyr		
385					390					395				400			
TCT	GAT	CTA	GTC	GTT	CCC	GAG	ATT	GAT	AAA	CGG	TTA	ATC	CAA	CTT	CAG		1248
Ser	Asp	Leu	Val	Val	Pro	Glu	Ile	Asp	Lys	Arg	Leu	Ile	Gln	Leu	Gln		
				405					410					415			
CTA	GAT	ATC	GCA	GCG	ATA	CAA	GAA	CAA	ACA	CCA	GAA	GAA	AAA	GCC	CTT		1296
Leu	Asp	Ile	Ala	Ala	Ile	Gln	Glu	Gln	Thr	Pro	Glu	Glu	Lys	Ala	Leu		
			420					425					430				
CAA	GAG	TTA	GAT	ACC	GAA	GAT	CAG	CGT	CAT	TTA	TAT	CTG	ATG	CTG	AAA		1344
Gln	Glu	Leu	Asp	Thr	Glu	Asp	Gln	Arg	His	Leu	Tyr	Leu	Met	Leu	Lys		
		435					440					445					
GAG	GAT	TAC	GAT	TCA	AGC	CTG	TTA	ATT	CCC	ACT	ATT	AAA	AAA	GCG	TTT		1392
Glu	Asp	Tyr	Asp	Ser	Ser	Leu	Leu	Ile	Pro	Thr	Ile	Lys	Lys	Ala	Phe		
	450					455					460						

AGC CAG AAT CCA ACG ATG ACA AGA CAA AAG TTA CTG CCT CTT GTT TTG Ser Gln Asn Pro Thr Met Thr Arg Gln Lys Leu Leu Pro Leu Val Leu 465 470 475 480	1440
CAG TGG TTG ATG GAA GGC GAA ACG GTA GTG TCA GAA CTA GAA AAG CCC Gln Trp Leu Met Glu Gly Glu Thr Val Val Ser Glu Leu Glu Lys Pro 485 490 495	1488
TCC AAG AGT AAA AAG GTT TCG GCT ATA AAG GTA GTC AAG CCC AGC GAC Ser Lys Ser Lys Lys Val Ser Ala Ile Lys Val Val Lys Pro Ser Asp 500 505 510	1536
TGG GAT AGC TTG CCT GAT ACG GAT TTA CGT TAT ATC TAT TCA CAA CGC Trp Asp Ser Leu Pro Asp Thr Asp Leu Arg Tyr Ile Tyr Ser Gln Arg 515 520 525	1584
CAA CCT GAA AAA ACC ATG CAT GAA CGG TTA AAA GGG AAA GGG GTA ATA Gln Pro Glu Lys Thr Met His Glu Arg Leu Lys Gly Lys Gly Val Ile 530 535 540	1632
GTG GAT ATG GCG AGC TTA TTT AAA CAA GCA GGT TAG CC Val Asp Met Ala Ser Leu Phe Lys Gln Ala Gly * 545 550 555	1670

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 556 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Ala Thr Arg Ile Gln Ala Val Tyr Arg Asp Thr Gly Val Glu 1 5 10 15
Ala Tyr Arg Asp Asn Pro Phe Ile Glu Ala Leu Pro Pro Leu Gln Glu 20 25 30
Ser Val Asn Ser Ala Ala Ser Leu Lys Ser Ser Leu Gln Leu Thr Ser 35 40 45
Ser Asp Leu Gln Lys Ser Arg Val Ile Arg Ala His Thr Ile Cys Arg 50 55 60
Ile Pro Asp Asp Tyr Phe Gln Pro Leu Gly Thr His Leu Leu Leu Ser 65 70 75 80
Glu Arg Ile Ser Val Met Ile Arg Gly Gly Tyr Val Gly Arg Asn Pro 85 90 95
Lys Thr Gly Asp Leu Gln Lys His Leu Gln Asn Gly Tyr Glu Arg Val 100 105 110

Gln Thr Gly Glu Leu Glu Thr Phe Arg Phe Glu Glu Ala Arg Ser Thr
 115 120 125
 Ala Gln Ser Leu Leu Leu Ile Gly Cys Ser Gly Ser Gly Lys Thr Thr
 130 135 140
 Ser Leu His Arg Ile Leu Ala Thr Tyr Pro Gln Val Ile Tyr His Arg
 145 150 155 160
 Glu Leu Asn Val Glu Gln Val Val Tyr Leu Lys Ile Asp Cys Ser His
 165 170 175
 Asn Gly Ser Leu Lys Glu Ile Cys Leu Asn Phe Phe Arg Ala Leu Asp
 180 185 190
 Arg Ala Leu Gly Ser Asn Tyr Glu Arg Arg Tyr Gly Leu Lys Arg His
 195 200 205
 Gly Ile Glu Thr Met Leu Ala Leu Met Ser Gln Ile Ala Asn Ala His
 210 215 220
 Ala Leu Gly Leu Leu Val Ile Asp Glu Ile Gln His Leu Ser Arg Ser
 225 230 235 240
 Arg Ser Gly Gly Ser Gln Glu Met Leu Asn Phe Phe Val Thr Met Val
 245 250 255
 Asn Ile Ile Gly Val Pro Val Met Leu Ile Gly Thr Pro Lys Ala Arg
 260 265 270
 Glu Ile Phe Glu Ala Asp Leu Arg Ser Ala Arg Arg Gly Ala Gly Phe
 275 280 285
 Gly Ala Ile Phe Trp Asp Pro Ile Gln Gln Thr Gln Arg Gly Lys Pro
 290 295 300
 Asn Gln Glu Trp Ile Ala Phe Thr Asp Asn Leu Trp Gln Leu Gln Leu
 305 310 315 320
 Leu Gln Arg Lys Asp Ala Leu Leu Ser Asp Glu Val Arg Asp Val Trp
 325 330 335
 Tyr Glu Leu Ser Gln Gly Val Met Asp Ile Val Val Lys Leu Phe Val
 340 345 350
 Leu Ala Gln Leu Arg Ala Leu Ala Leu Gly Asn Glu Arg Ile Thr Ala
 355 360 365
 Gly Leu Leu Arg Gln Val Tyr Gln Asp Glu Leu Lys Pro Val His Pro
 370 375 380
 Met Leu Glu Ala Leu Arg Ser Gly Ile Pro Glu Arg Ile Ala Arg Tyr
 385 390 395 400
 Ser Asp Leu Val Val Pro Glu Ile Asp Lys Arg Leu Ile Gln Leu Gln
 405 410 415
 Leu Asp Ile Ala Ala Ile Gln Glu Gln Thr Pro Glu Glu Lys Ala Leu

420	425	430
Gln Glu Leu Asp Thr Glu Asp	Gln Arg His Leu Tyr	Leu Met Leu Lys
435	440	445
Glu Asp Tyr Asp Ser Ser	Leu Leu Ile Pro Thr	Ile Lys Lys Ala Phe
450	455	460
Ser Gln Asn Pro Thr Met	Thr Arg Gln Lys	Leu Leu Pro Leu Val Leu
465	470	475
Gln Trp Leu Met Glu Gly	Glu Thr Val Val	Ser Glu Leu Glu Lys Pro
485	490	495
Ser Lys Ser Lys Lys Val	Ser Ala Ile Lys Val	Val Lys Pro Ser Asp
500	505	510
Trp Asp Ser Leu Pro Asp	Thr Asp Leu Arg Tyr	Ile Tyr Ser Gln Arg
515	520	525
Gln Pro Glu Lys Thr Met	His Glu Arg Leu Lys	Gly Lys Gly Val Ile
530	535	540
Val Asp Met Ala Ser Leu	Phe Lys Gln Ala Gly	*
545	550	555

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5926 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "pEM delta R.adj to 1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTTAGAGCAA TTCGGTGTTA GTTTCAGCAA GCAAACATTA ACCATAGCTA ATGATTTATA	60
GCCATATTAA CCATTGGGGT ACCGAGCTCG AATTCCATGG TCTGTTTCCT GTGTGAAATT	120
GTTATCCGCT CACAATTCCA CACATTATAC GAGCCGGATG ATTAATTGTC AACAGCTCAT	180
TTCAGAATAT TTGCCAGAAC CGTTATGATG TCGGCGCAAA AAACATTATC CAGAACGGGA	240
GTGCGCCTTG AGCGACACGA ATTATGCAGT GATTTACGAC CTGCACAGCC ATACCACAGC	300
TTCCGATGGC TGCCTGACGC CAGAAGCATT GGTGCACCGT GCAGTCGATG ATAAGCTGTC	360
AAACCAGATC AATTGCGGCT AACTCACATT AATTGCGTTG CGCTCACTGC CCGCTTTCCA	420
GTCGGGAAAC CTGTCTGTGCC AGCTGCATTA ATGAATCGGC CAACGCGCGG GGAGAGGCGG	480

TTTGCGTATT GGGCGCCAGG GTGGTTTTTC TTTTCACCAG TGAGACGGGC AACAGCTGAT 540
 TGCCCTTCAC CGCCTGGCCC TGAGAGAGTT GCAGCAAGCG GTCCACGCTG GTTTGCCCCA 600
 GCAGGCGAAA ATCCTGTTTG ATGGTGGTTG ACGGCGGGAT ATAACATGAG CTGTCTTCGG 660
 TATCGTCGTA TCCCACTACC GAGATATCCG CACCAACGCG CAGCCCGGAC TCGGTAATGG 720
 CGCGCATTGC GCCCAGCGCC ATCTGATCGT TGGCAACCAG CATCGCAGTG GGAACGATGC 780
 CCTCATTCAG CATTTGCATG GTTTGTTGAA AACC GGACAT GGC ACTCCAG TCGCCTTCCC 840
 GTTCCGCTAT CGGCTGAATT TGATTGCGAG TGAGATATTT ATGCCAGCCA GCCAGACGCA 900
 GACGCGCCGA GACAGAACTT AATGGGCCCC CTAACAGCGC GATTGCTGG TGACCCAATG 960
 CGACCAGATG CTCCACGCCC AGTCGCGTAC CGTCTTCATG GGAGAAAATA ATACTGTTGA 1020
 TGGGTGTCTG GTCAGAGACA TCAAGAAATA ACGCCGGAAC ATTAGTGCAG GCAGCTTCCA 1080
 CAGCAATGGC ATCCTGGTCA TCCAGCGGAT AGTTAATGAT CAGCCCACTG ACGCGTTGCG 1140
 CGAGAAGATT GTGCACCGCC GCTTTACAGG CTTCGACGCC CCTTCGTTCT ACCATCGACA 1200
 CCACCACGCT GGCACCCAGT TGATCGGCGC GAGATTTAAT CGCCGCGACA ATTTGCGACG 1260
 GCGCGTGCAG GGCCAGACTG GAGGTGGCAA CGCCAATCAG CAACGACTGT TTGCCCCCCA 1320
 GTTGTGTGTC CACGCGGTTG GGAATGTAAT TCAGCTCCGC CATCGCCGCT TCCAATTTTT 1380
 CCCGCGTTTT CGCAGAAACG TGGCTGGCCT GGTTCACCAC GCGGGAAACG GTCTGATAAG 1440
 AGACACCGGC ATACTCTGCG ACATCGTATA ACGTTACTGG TTTCACATTC ACCACCCTGA 1500
 ATTGACTCTC TTCCGGGCGC TATCATGCCA TACCGCGAAA GGTTTTGCAC CATTCGATGG 1560
 TGTCAACGTA AATGCATGCC GCTTCGCCTT CGCGCGCGAA TTGATCTGCT GCCTCGCGCG 1620
 TTTCCGGTGAT GACGGTGAAA ACCTCTGACA CATGCAGCTC CCGGAGACGG TCACAGCTTG 1680
 TCTGTAAGCG GATGCCGGGA GCAGACAAGC CCGTCAGGGC GCGTCAGCGG GTGTTGGCGG 1740
 GTGTCGGGGC GCAGCCATGA CCCAGTCAG TAGCGATAGC GGAGTGTATA CTGGCTTAAC 1800
 TATGCGGCAT CAGAGCAGAT TGTACTGAGA GTGCACCATA TGCGGTGTGA AATACCGCAC 1860
 AGATGCGTAA GGAGAAAATA CCGCATCAGG CGCTCTTCCG CTTCCTCGCT CACTGACTCG 1920
 CTGCGCTCGG TCGTTCGGCT GCGGCGAGCG GTATCAGCTC ACTCAAAGGC GGTAATACGG 1980
 TTATCCACAG AATCAGGGGA TAACGCAGGA AAGAACATGT GAGCAAAAGG CCAGCAAAAG 2040
 GCCAGGAACC GTAAAAAGGC CGCGTTGCTG GCGTTTTTCC ATAGGCTCCG CCCCCCTGAC 2100
 GAGCATCACA AAAATCGACG CTCAAGTCAG AGGTGGCGAA ACCCGACAGG ACTATAAAGA 2160
 TACCAGGCGT TTCCCCCTGG AAGCTCCCTC GTGCGCTCTC CTGTTCCGAC CCTGCCGCTT 2220

ACCGGATACC TGTCCGCCTT TCTCCCTTCG GGAAGCGTGG CGCTTTCTCA TAGCTCACGC 2280
 TGTAGGTATC TCAGTTCGGT GTAGGTCGTT CGCTCCAAGC TGGGCTGTGT GCACGAACCC 2340
 CCCGTTTCAGC CCGACCGCTG CGCCTTATCC GGTAACATATC GTCTTGAGTC CAACCCGGTA 2400
 AGACACGACT TATCGCCACT GGCAGCAGCC ACTGATAACA GGATTAGCAG AGCGAGGTAT 2460
 GTAGGCGGTG CTACAGAGTT CTTGAAGTGG TGGCCTAACT ACGGCTACAC TAGAAGGACA 2520
 GTATTTGGTA TCTGCGCTCT GCTGAAGCCA GTTACCTTCG GAAAAAGAGT TGGTAGCTCT 2580
 TGATCCGGCA AACAAACCAC CGCTGGTAGC GGTGGTTTTT TTGTTTGCAA GCAGCAGATT 2640
 ACGCGCAGAA AAAAAGGATC TCAAGAAGAT CCTTTGATCT TTTCTACGGG GTCTGACGCT 2700
 CAGTGAACG AAAACTCACG TTAAGGAGTT TTGGTCATGA GATTATCAAA AAGGATCTTC 2760
 ACCTAGATCC TTTTAAATTA AAAATGAAGT TTTAAATCAA TCTAAAGTAT ATATGAGTAA 2820
 ACTTGGTCTG ACAGTTACCA ATGCTTAATC AGTGAGGCAC CTATCTCAGC GATCTGTCTA 2880
 TTTTCGTTTAT CCATAGTTGC CTGACTCCCC CTCGTGTAGA TAACTACGAT ACGGGAGGGC 2940
 TTACCATCTG GCCCCAGTGC TGCAATGATA CCGCGAGACC CACGCTCACC GGCTCCAGAT 3000
 TTATCAGCAA TAAACCAGCC AGCCGGAAGG GCGGAGCGCA GAAGTGGTCC TGCAACTTTA 3060
 TCCGCCTCCA TCCAGTCTAT TAATTGTTGC CCGGAAGCTA GAGTAAGTAG TTCGCCAGTT 3120
 AATAGTTTGC GCAACGTTGT TGCCATTGCT GTAGGCATCG TGGTGTACAG CTCGTCTGTT 3180
 GGTATGGCTT CATTAGCTC CGGTTCCTAA CGATCAAGGC GAGTTACATG ATCCCCCATG 3240
 TTGTGCAAAA AAGCGGTTAG CTCCTTCGGT CCTCCGATCG TTGTCAGAAG TAAATTGGCC 3300
 GCAGTGTTAT CACTCATGGT TATGGCAGCA CTGCATAATT CTCTTACTGT CATGCCATCC 3360
 GTAAGATGCT TTTCTGTGAC TGGTGAGTAC TCAACCAAGT CATTCTGAGA ATAGTGTATG 3420
 CGGCGACCGA GTTGCTCTTG CCCGGCGTCA ACACGGGATA ATACCGCGCC ACATAGCAGA 3480
 ACTTTAAAAG TGCTCATCAT TGAACACGT TCTTCGGGGC GAAAACTCTC AAGGATCTTA 3540
 CCGCTGTTGA GATCCAGTTC GATGTAACCC ACTCGTGCAC CCAACTGATC TTCAGCATCT 3600
 TTTACTTTCA CCAGCGTTTC TGGGTGAGCA AAAACAGGAA GGCAAAATGC CGCAAAAAAG 3660
 GGAATAAGGG CGACACGGAA ATGTTGAATA CTCATACTCT TCCTTTTCA ATATTATTGA 3720
 AGCATTTATC AGGGTTATTG TCTCATGAGC GGATACATAT TTGAATGTAT TTAGAAAAAT 3780
 AAACAAAAAG AGTTTGTAGA AACGCAAAAA GGCCATCCGT CAGGATGGCC TTCTGCTTAA 3840
 TTTGATGCCT GGCAGTTTAT GCGGGGCGTC CTGCCCCCA CCCTCCGGGC CGTTGCTTCG 3900
 CAACGTTCAA ATCCGCTCCC GCGGATTG TCCTACTCAG GAGAGCGTTC ACCGACAAAC 3960

AACAGATAAA ACGAAAGGCC CAGTCTTTCG ACTGAGCCTT TCGTTTTATT TGATGCCTGG 4020
CAGTTCCTTA CTCTCGCATG GGGAGACCCC AACTACCAT CGGCGCTACG GCGTTTCACT 4080
TCTGAGTTCG GCATGGGGTC AGGTGGGACC ACCGCGCTAC TGCCGCCAGG CAAATTCTGT 4140
TTTATCAGAC CGCTTCTGCG TTCTGATTTA ATCTGTATCA GGCTGAAAAT CTTCTCTCAT 4200
CCGCCAAAAC AGCCAAGCTT GCATGCCTGC AGGTGCACTC TAGAGGATCC CCAAGAAAGT 4260
CCGTGCGACA GCTTTAATAA ACCCTGCACT TATCTGTTTA GTGTGGGCGG ACAAATAGT 4320
TGGGAACCTGG GAGGGGTGGA AATGGAGTTT TTAAGGATTA TTTAGGGAAG AGTGACAAAA 4380
TAGATGGGAA CTGGGTGTAG CGTCGTAAGC TAATACGAAA ATTAAAAATG ACAAATAGT 4440
TTGGAACCTAG ATTTCACTTA TCTGTTGGT CGACCTGCAG GGGGGGGGGG GAAAGCCACG 4500
TTGTGTCTCA AAATCTCTGA TGTTACATTG CACAAGATAA AAATATATCA TCATGAACAA 4560
TAAAACTGTC TGCTTACATA AACAGTAATA CAAGGGGTGT TATGAGCCAT ATTCAACGGG 4620
AAACGTCTTG CTCGAGGCCG CGATTAAATT CCAACATGGA TGCTGATTTA TATGGGTATA 4680
AATGGGCTCG CGATAATGTC GGGCAATCAG GTGCGACAAT CTATCGATTG TATGGGAAGC 4740
CCGATGCGCC AGAGTTGTTT CTGAAACATG GCAAAGGTAG CGTTGCCAAT GATGTTACAG 4800
ATGAGATGGT CAGACTAAAC TGGCTGACGG AATTTATGCC TCTTCCGACC ATCAAGCATT 4860
TTATCCGTAC TCCTGATGAT GCATGGTTAC TCACCACTGC GATCCCCGGG AAAACAGCAT 4920
TCCAGGTATT AGAAGAATAT CCTGATTGAG GTGAAAATAT TGTTGATGCG CTGGCAGTGT 4980
TCCTGCGCCG GTTGCAATTCG ATTCCTGTTT GTAATTGTCC TTTTAACAGC GATCGCGTAT 5040
TTCGTCTCGC TCAGGCGCAA TCACGAATGA ATAACGGTTT GGTGATGCG AGTGATTTTG 5100
ATGACGAGCG TAATGGCTGG CCTGTTGAAC AAGTCTGGAA AGAAATGCAT AAGCTTTTGC 5160
CATTCTCACC GGATTCAGTC GTCACATG GTGATTTCTC ACTTGATAAC CTTATTTTGT 5220
ACGAGGGGAA ATTAATAGGT TGTATTGATG TTGGACGAGT CGGAATCGCA GACCGATACC 5280
AGGATCTTGC CATCCTATGG AACTGCCTCG GTGAGTTTTC TCCTTCATTA CAGAAACGGC 5340
TTTTTCAAAA ATATGGTATT GATAATCCTG ATATGAATAA ATTGCAGTTT CATTTGATGC 5400
TCGATGAGTT TTTCTAATCA GAATTGGTTA ATTGGTTGTA AACTGGCAG AGCATTACGC 5460
TGACTTGACG GGACGGCGGC TTTGTTGAAT AAATCGAACT TTTGCTGAGT TGAAGGATCA 5520
GATCACGCAT CTTCCCGACA ACGCAGACCG TTCCGTGGCA AAGCAAAAGT TCAAAATCAC 5580
CAACTGGTCC ACCTACAACA AAGCTCTCAT CAACCGTGGC TCCCTCACTT TCTGGCTGGA 5640
TGATGGGGCG ATTCAGGCCT GGTATGAGTC AGCAACACCT TCTTCACGAG GCAGACCTCA 5700

GCGCCCCCCC CCCCCTGCAG GTCGACCCCA CGCCCCTCTT TAATACGACG GGCAATTTGC 5760
 ACTTCAGAAA ATGAAGAGTT TGCTTTAGCC ATAACAAAAG TCCAGTATGC TTTTTCACAG 5820
 CATAACTGGA CTGATTTTCAG TTTACAATA TTCTGTCTAG TTTAAGACTT TATTGTCATA 5880
 GTTTAGATCT ATTTTGTTC A GTTTAAGACT TTATTGTCCG CCCACA 5926

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5926 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "pEM-delta"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAGATCAATT CGCGCTAACT CACATTAATT GCGTTGCGCT CACTGCCCCG TTTCCAGTCG 60
 GGAAACCTGT CGTGCCAGCT GCATTAATGA ATCGGCCAAC GCGCGGGGAG AGGCGGTTTG 120
 CGTATTGGGC GCCAGGGTGG TTTTCTTTT CACCAGTGAG ACGGGCAACA GCTGATTGCC 180
 CTTACCGGCC TGGCCCTGAG AGAGTTGCAG CAAACGGTCC ACGCTGGTTT GCCCCAGCAG 240
 GCGAAAATCC TGTTTGATGG TSGTTGACGG CGGGATATAA CATGAGCTGT CTTCGGTATC 300
 GTCGTATCCC ACTACCGAGA TATCCGCACC AACCGGCAGC CCGGACTCGG TAATGGCGCG 360
 CATTGCGCCC AGCGCCATCT GATCGTTGGC AACCAGCATC GCAGTGGGAA CGATGCCCTC 420
 ATTCAGCATT TGCATGGTTT GTTGAAAACC GGACATGGCA CTCCAGTCGC CTTCCCGTTC 480
 CGCTATCGGC TGAATTTGAT TGCGAGTGAG ATATTTATGC CAGCCAGCCA GACGCAGACG 540
 CGCCGAGACA GAACTTAATG GGCCCGCTAA CAGCGCGATT TGCTGGTGAC CCAATGCGAC 600
 CAGATGCTCC ACGCCCAGTC GCGTACCGTC TTCATGGGAG AAAATAATAC TGTGATGGG 660
 TGTCTGGTCA GAGACATCAA GAAATAACGC CGGAACATTA GTGCAGGCAG CTTCCACAGC 720
 AATGGCATCC TGGTCATCCA GCGGATAGTT AATGATCAGC CCACTGACGC GTTGCGCGAG 780
 AAGATTGTGC ACCGCCGCTT TACAGGCTTC GACGCCGCTT CGTTCTACCA TCGACACCAC 840
 CACGCTGGCA CCCAGTTGAT CGGCGCGAGA TTTAATCGCC GCGACAATTT GCGACGGCGC 900
 GTGCAGGGCC AGACTGGAGG TGGCAACGCC AATCAGCAAC GACTGTTTGC CCGCCAGTTG 960
 TTGTGCCACG CGGTTGGGAA TGTAATTCAG CTCCGCCATC GCCGCTTCCA CTTTTTCCCG 1020

CGTTTTTCGCA GAAACGTGGC TGGCCTGGTT CACCACGCGG GAAACGGTCT GATAAGAGAC 1080
ACCGGCATAC TCTGCGACAT CGTATAACGT TACTGGTTTC ACATTCACCA CCCTGAATTG 1140
ACTCTCTTCC GGGCGCTATC ATGCCATACC GCGAAAGGTT TTGCACCATT CGATGGTGTG 1200
AACGTAAATG CATGCCGCTT CGCCTTCGCG CGCGAATTGA TCTGCTGCCT CGCGCGTTTC 1260
GGTGATGACG GTGAAAACCT CTGACACATG CAGCTCCCGG AGACGGTCAC AGCTTGTCTG 1320
TAAGCGGATG CCGGGAGCAG ACAAGCCCGT CAGGGCGCGT CAGCGGGTGT TGGCGGGTGT 1380
CGGGGCGCAG CCATGACCCA GTCACGTAGC GATAGCGGAG TGTATACTGG CTTAACTATG 1440
CGGCATCAGA GCAGATTGTA CTGAGAGTGC ACCATATGCG GTGTGAAATA CCGCACAGAT 1500
GCGTAAGGAG AAAATACCGC ATCAGGCGCT CTTCCGCTTC CTCGCTCACT GACTCGCTGC 1560
GCTCGGTCGT TCGGCTGCGG CGAGCGGTAT CAGCTCACTC AAAGGCGGTA ATACGGTTAT 1620
CCACAGAATC AGGGGATAAC GCAGGAAAGA ACATGTGAGC AAAAGGCCAG CAAAAGGCCA 1680
GGAACCGTAA AAAGGCGCGG TTGCTCCCGT TTTTCCATAG GCTCCGCCCC CCTGACGAGC 1740
ATCACAAAAA TCGACGCTCA AGTCAGAGGT GCGGAAACCC GACAGGACTA TAAAGATACC 1800
AGGCGTTTTCC CCCTGGAAGC TCCCTCGTGC GCTCTCCTGT TCCGACCCTG CCGCTTACCG 1860
GATACCTGTC CGCCTTTCTC CCTTCGGGAA GCGTGGCGCT TTCTCATAGC TCACGCTGTA 1920
GGTATCTCAG TTCGGTGTAG GTCGTTGCT CCAAGCTGGG CTGTGTGCAC GAACCCCCCG 1980
TTCAGCCCCG CCGCTGCGCC TTATCCGGTA ACTATCGTCT TGAGTCCAAC CCGGTAAGAC 2040
ACGACTTATC GCCACTGGCA GCAGCCACTG GTAACAGGAT TAGCAGAGCG AGGTATGTAG 2100
GCGGTGCTAC AGAGTTCTTG AAGTGGTGGC CTAACACGG CTACACTAGA AGGACAGTAT 2160
TTGGTATCTG CGCTCTGCTG AAGCCAGTTA CCTTCGGAAA AAGAGTTGGT AGCTCTTGAT 2220
CCGGCAAACA AACCACCGCT GGTAGCGGTG GTTTTTTTGT TTGCAAGCAG CAGATTACGC 2280
GCAGAAAAAA AGGATCTCAA GAAGATCCTT TGATCTTTTC TACGGGGTCT GACGCTCAGT 2340
GGAACGAAAA CTCACGTAA GGGATTTTGG TCATGAGATT ATCAAAAAGG ATCTTCACCT 2400
AGATCCTTTT AAATTAAAAA TGAAGTTTAA AATCAATCTA AAGTATATAT GAGTAAACTT 2460
GGTCTGACAG TTACCAATGC TTAATCAGTG AGGCACCTAT CTCAGCGATC TGTCTATTTC 2520
GTTTCATCCAT AGTTGCCTGA CTCCCCGTCG TGTAGATAAC TACGATACGG GAGGGCTTAC 2580
CATCTGGCCC CAGTGCTGCA ATGATACCGC GAGACCCACG CTCACCGGCT CCAGATTTAT 2640
CAGCAATAAA CCAGCCAGCC GGAAGGGCCG AGCGCAGAAG TGGTCCTGCA ACTTTATCCG 2700
CCTCCATCCA GTCTATTAAT TGTTGCCGGG AAGCTAGAGT AAGTAGTTTC CCAGTTAATA 2760

GTTTGCGCAA CGTTGTTGCC ATTGCTGTAG GCATCGTGGT GTCACGCTCG TCGTTTGGTA 2820
 TGGCTTCATT CAGCTCCGGT TCCCAACGAT CAAGGCGAGT TACATGATCC CCCATGTTGT 2880
 GCAAAAAAGC GGTTAGCTCC TTCGGTCCTC CGATCGTTGT CAGAAGTAAG TTGGCCGCAG 2940
 TGTTATCACT CATGGTTATG GCAGCACTGC ATAATTCTCT TACTGTCATG CCATCCGTAA 3000
 GATGCTTTTC TGTGACTGGT GAGTACTCAA CCAAGTCATT CTGAGAATAG TGTATGCGGC 3060
 GACCGAGTTG CTCTTGCCCG GCGTCAACAC GGGATAATAC CGCGCCACAT AGCAGAACTT 3120
 TAAAAGTGCT CATCATTGGA AAACGTTCTT CGGGGCGAAA ACTCTCAAGG ATCTTACCGC 3180
 TGTTGAGATC CAGTTCGATG TAACCCACTC GTGCACCCAA CTGATCTTCA GCATCTTTTA 3240
 CTTTCACCAg CGTTTCTGGG TGAGCAAAAA CAGGAAGGCA AAATGCCGCA AAAAAGGGAA 3300
 TAAGGGCGAC ACGGAAATGT TGAATACTCA TACTCTTCCT TTTCAATAT TATTGAAGCA 3360
 TTTATCAGGG TTATTGTCTC ATGAGCGGAT ACATATTTGA ATGTATTTAG AAAAATAAAC 3420
 AAAAAGAGTT TGTAGAAACG CAAAAGGCC ATCCGTCAGG ATGGCCTTCT GCTTAATTTG 3480
 ATGCCTGGCA GTTTATGGCG GCGTCTCTGC CCGCCACCCT CCGGGCCGTT GCTTCGCAAC 3540
 GTTCAAATCC GCTCCCGGCG GATTTGTCTT AATCAGGAGA GCGTTCACCG ACAAACAACA 3600
 GATAAAACGA AAGGCCCACT CTTTCGACTG AGCCTTTCGT TTTATTTGAT GCCTGGCAGT 3660
 TCCCTACTCT CGCATGGGGA GACCCCAAC TACCATCGGC GCTACGGCGT TTCCTTCTG 3720
 AGTTCGGCAT GGGGTCAGGT GGGACCACCG CBTACTGCC GCCAGGCAAA TTCTGTTTAA 3780
 TCAGACCGCT TCTGCGTTCT GATTAAATCT GTATCAGGCT GAAAATCTTC TCTCATCCGC 3840
 CAAAACAGCC AAGCTTGCAT GCCTGCAGST CGACTCTAGA GGATCCCCAA GAAAGTCCGT 3900
 CGGACAGCTT TAATAAACCC TGCACTTATC TGTTTAGTGT GGGCGGACAA AATAGTTGGG 3960
 AACTGGGAGG GGTGGAAATG GAGTTTTTAA GGATTATTTA GGGAAAGAGTG ACAAATAGA 4020
 TGGGAAGTGG GTGTAGCGTC GTAAGCTAAT ACGAAAATTA AAAATGACAA AATAGTTTGG 4080
 AACTAGATTT CACTTATCTG GTTGGTCTGAC CTGCAGGGGG GGGGGGGAAA GCCACGTTGT 4140
 GTCTCAAAAT CTCTGATGTT ACATTGACAA AGATAAAAAAT ATATCATCAT GAACAATAAA 4200
 ACTGTCTGCT TACATAAACA GTAATAAAG GGGTGTTATG AGCCATATTC AACGGGAAAC 4260
 GTCTTGCTCG AGGCCGCGAT TAAATTCCAA CATGGATGCT GATTTATATG GGTATAAATG 4320
 GGCTCGCGAT AATGTGCGGC AATCAGGTGC GACAATCTAT CGATTGTATG GGAAGCCCGA 4380
 TGCGCCAGAG TTGTTTCTGA AACATGGCAA AGGTAGCGTT GCCAATGATG TTACAGATGA 4440
 GATGGTCAGA CTAAACTGGC TGACGGAATT TATGCCTCTT CCGACCATCA AGCATTTTAT 4500

CCGTACTCCT GATGATGCAT GGTTACTCAC CACTGCGATC CCCGGGAAAA CAGCATTCCA 4560
 GGTATTAGAA GAATATCCTG ATTCAGGTGA AAATATTGTT GATGCGCTGG CAGTGTTCCT 4620
 GCGCCGGTTG CATTGATTG CTGTTTGTA TGTCCCTTT AACAGCGATC GCGTATTTG 4680
 TCTCGCTCAG GCGCAATCAC GAATGAATAA CGTTTGGTT GATGCGAGTG ATTTTGATGA 4740
 CGAGCGTAAT GGCTGGCCTG TTGAACAAGT CTGGAAAGAA ATGCATAAGC TTTTGCCATT 4800
 CTCACCGGAT TCAGTCGTCA CTCATGGTGA TTTCTCACTT GATAACCTTA TTTTGACGA 4860
 GGGGAAATTA ATAGGTTGTA TTGATGTTGG ACGAGTCGGA ATCGCAGACC GATACCAGGA 4920
 TCTTGCCATC CTATGGAAC TCCCTGGTGA GTTTTCTCCT TCATTACAGA AACGGCTTTT 4980
 TCAAAAATAT GGTATTGATA ATCCTGATAT GAATAAATTG CAGTTTCATT TGATGCTCGA 5040
 TGAGTTTTTC TAATCAGAAT TGGTTAATTG GTTGTAACAC TGGCAGAGCA TTACGCTGAC 5100
 TTGACGGGAC GGCGGCTTTG TTGAATAAAT CGAACTTTTG CTGAGTTGAA GGATCAGATC 5160
 ACGCATCTTC CCGACAACGC AGACCGTTCC GTGGCAAAGC AAAAGTTCAA AATCACCAAC 5220
 TGGTCCACCT ACAACAAAGC TCTCATCAAC CGTGGCTCCC TCACTTTCTG GCTGGATGAT 5280
 GGGGCGATTG AGGCCTGGTA TGAGTCAGCA ACACCTTCTT CACGAGGCAG ACCTCAGCGC 5340
 CCCCCCCCCC CTGCAGGTCG ACCCCACGCC CCTCTTTAAT ACGACGGGCA ATTTGCACTT 5400
 CAGAAAATGA AGAGTTTGCT TTAGCCATAA CAAAAGTCCA GTATGCTTTT TCACAGCATA 5460
 ACTGGACTGA TTTTCAGTTT CAACTATTCT GTCTAGTTTA AGACTTTATT GTCATAGTTT 5520
 AGATCTATTT TGTTCAGTTT AAGACTTTAT TGTCCGCCCA CATTTAGAGC AATTCGGTGT 5580
 TAGTTTCAGC AAGCAAACAT TAACCATAGC TAATGATTTA TAGCCATATT AACCATTGGG 5640
 GTACCGAGCT CGAATTCCAT GGTCTGTTT CTGTGTGAAA TTGTTATCCG CTCACAATTC 5700
 CACACATTAT ACGAGCCGGA TGATTAATTG TCAACAGCTC ATTTCAGAAT ATTTGCCAGA 5760
 ACCGTTATGA TGTCGGCGCA AAAAACATTA TCCAGAACGG GAGTGCGCCT TGAGCGACAC 5820
 GAATTATGCA GTGATTTACG ACCTGCACAG CCATACCACA GCTTCCGATG GCTGCCTGAC 5880
 GCCAGAAGCA TTGGTGCACC GTGCAGTCGA TGATAAGCTG TCAAAC 5926

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8906 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "pER183 (target plasmid)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCCGGA TGAGCATTCA TCAGGCGGGC AAGAATGTGA ATAAAGGCCG GATAAACTT 60
GTGCTTATTT TTCTTTACGG TCTTTAAAAA GGCCGTAATA TCCAGCTGAA CGGTCTGGTT 120
ATAGGTACAT TGAGCAACTG ACTGAAATGC CTCAAAATGT TCTTTACGAT GCCATTGGGA 180
TATATCAACG GTGGTATATC CAGTGATTTT TTTCTCCATT TTAGCTTCCT TAGCTCCTGA 240
AAATCTCGAT AACTCAAAAA ATACGCCCGG TAGTGATCTT ATTTCAATTAT GGTGAAAGTT 300
GGAACCTCTT ACGTGCCGAT CAACGTCTCA TTTTCGCCAA AAGTTGGCCC AGGGCTTCCC 360
GGTATCAACA GGGACACCAG GATTTATTTA TTCTGCGAAG TGATCTTCCG TCACAGGTAT 420
TTATTCGGCG CAAAGTGCGT CGGGTGATGC TGCCAACTTA CTGATTTAGT GTATGATGGT 480
GTTTTTGAGG TGCTCCAGTG GCTTCTGTTT CTATCAGCTG TCCCTCCTGT TCAGCTACTG 540
ACGGGGTGGT GCGTAACGGC AAAAGCACCG CCGGACATCA GCGCTAGCGG AGTGTATACT 600
GGCTTACTAT GTTGGCACTG ATGAGGGTGT CAGTGAAGTG CTTCATGTGG CAGGAGAAAA 660
AAGGCTGCAC CGGTGCGTCA GCAGAATATG TGATACAGGA TATATTCCGC TTCCTCGCTC 720
ACTGACTCGC TACGCTCGGT CGTTCGACTG CCGCGAGCGG AAATGGCTTA CGAACGGGGC 780
GGAGATTTCC TGGAAGATGC CAGGAAGATA CTTAACAGGG AAGTGAGAGG GCCGCGGCAA 840
AGCCGTTTTT CCATAGGCTC CGCCCCCTG ACAAGCATCA CGAAATCTGA CGCTCAAATC 900
AGTGGTGGCG AAACCCGACA GGA CTATAAA GATACCAGGC GTTTCCCTG GCGGCTCCCT 960
CGTGCGCTCT CCTGTTCCCTG CCTTTCGGTT TACCGGTGTC ATTCCGCTGT TATGGCCGCG 1020
TTTGTCTCAT TCCACGCCTG AACTCAGTT CCGGGTAGGC AGTTCGCTCC AAGCTGGACT 1080
GTATGCACGA ACCCCCCGTT CAGTCCGACC GCTGCGCCTT ATCCGGTAAC TATCGTCTTG 1140
AGTCCAACCC GGAAAGACAT GCAAAAGCAC CACTGGCAGC AGCCACTGGT AATTGATTTA 1200
GAGGAGTTAG TCTTGAAGTC ATGCGCCGGT TAAGGCTAAA CTGAAAGGAC AAGTTTTGGT 1260
GACTGCGCTC CTCCAAGCCA GTTACCTCGG TTCAAAGAGT TGGTAGCTCA GAGAACCTTC 1320
GAAAAACCGC CTGCAAGGC GGTTTTTTCG TTTTCAGAGC AAGAGATTAC GCGCAGACCA 1380
AAACGATCTC AAGAAGATCA TCTTATTAAT CAGATAAAAT ATTTCTAGAT TTCAGTGCAA 1440
TTTATCTCTT CAAATGTAGC ACCTGAAGTC AGCCCCATAC GATATAAGTT GTAATTCTCA 1500
TGTTTGACAG CTTATCATCG GATGGATCTG AAATTGTAAA CGTTAATATT TTGTAAATT 1560

CGCGTTAAAT TTTTGTAA TACAGTCATT TTTTAACCAA TAGGCCGAAA TCGGCAAAAT 1620
CCCTTATAAA TCAAAAGAAT AGACCGAGAT AGGGTTGAGT GTTGTTCAG TTTGGAACAA 1680
GAGTCCACTA TTAAAGAACG TGGACTCCAA CGTCAAAGGG CGAAAAACCG TCTATCAGGG 1740
CGATGGCCCA CTACGTGAAC CATCACCCTA ATCAAGTTTT TTGGGGTCGA GGTGCCGTAA 1800
AGCACTAAAT CGGAACCCTA AAGGGAGCCC CCGATTTAGA GCTTGACGGG GAAAGCCGGC 1860
GAACGTGGCG AGAAAGGAAG GGAAGAAAGC GAAAGGAGCG GGCGCTAGGG CGCTGGCAAG 1920
TG TAGCGGTC ACGCTGCGCG TAACCACCAC ACCCGCCGCG CTTAATGCGC CGCTACAGGG 1980
CGCGTCAGAT CCCATCGATA AGCTTTAATG CGGTAGTTTA TCACAGTTAA ATTGCTAACG 2040
CAGTCAGGCA CCGTGTATGA AATCTAACAA TGCGCTCATC GTCATCCTCG GCACCGTCAC 2100
CCTGGATGCT GTAGGCATAG GCTTGGTTAT GCCGGTACTG CCGGGCCTCT TGCGGGATAT 2160
CGTCCATTCC GACAGCATCG CCAGTCACTA TGGCGTGCTG CTAGCGCTAT ATGCGTTGAT 2220
GCAATTTCTA TGCGCACCCG TTCTCGGACC ACTGTCCGAC CGCTTTGGCC GCCGCCCAGT 2280
CCTGCTCGCT TCGCTACTTG GAGCCACTAT CGACTACGCG ATCATGGCGA CCACACCCGT 2340
CCTGTGGATC CGCTGGCGAA AGGGGGATGT GCTGCAAGGC GATTAAGTTG GGTAACGCCA 2400
GGGTTTTCCC AGTCACGACG TTGTAAAACG ACGGCCAGTG AATTGCGGCC GCCCTGCAAG 2460
GAAGGGAATG TCGCCAACAG CGAAGAGAGT TGGGCAACGG ATGTGCTGST GGAGGTGATC 2520
GCCTCTGAT GATGAGCCGC TCCCGATGTG GTGTGCGGAG CGGTATTTTC TATAAACTT 2580
ACCGCTTATT TGAGATATTC ATCGAAAATG TCGAGTAATT CTTGATGTAT ACACGGCCAT 2640
TCCTGACCTA AATTGACGGT ACACAAGCCA ATATCGAAGC CATTAATTTT ATAACGATGT 2700
TTCACTGCGG TATCTACGTG GGGATATATT AATAACCCCC CTATGTTTTT GCCATTTTCA 2760
GGCTTTAACG ACCATAAGTA ATTCATCAGT TGATAAAGAT TTTGCGAATG AAATTTTTCT 2820
GTTCCCATTC GTCGTGAAAA AATGCTCTTA TAGTATTTGG CGTCAACGAT AAGTATTTTT 2880
TCTGATGAGC GAATGGTGAT GTCAGTTTCC ATTCGAGGTA ACAAATTAAG TGA CTGATCC 2940
GATATACTCG ATGCATCCCA TTTTAAATAA GAGCGGGTTG TGTTTG CAGA CGTTAATTCA 3000
CGACGGCAAA ATTCATAAAG AAACCTTTGA TAAAGTAATG ACATCTCTTT TTCGTTTCTT 3060
TCAAAATCAT AGAAACGGTA GTGTCCTTG TTTTGACCTG GAATAGAATT ATTGACGATG 3120
AATTTGCAGA CACTGATAAC GAATTTATAA TAACGCGTAT TTTTCCGCC ATTCAGATAG 3180
CTGAAATGCT GCGGAGTTAA ATGAAGAGTG CTAATGCCCG GTAATTTTCT ATAAAGTGAA 3240
CGAGCTTCAT CTCTGATAGT TGAATTTAAC TTTTCATGCT TAATTAATAT GGCTAATGTG 3300

CTTTTTATAA TTCGGTTAGC CAGCGTGTCT TCATTAAGCA TATCAAAAGT ACTGACGGTT 3360
 TTCCCATGAT TAAGATGGAA GCCGCGTATT GTTTTAGCAA ACTCTATTCG CCCTTTGATG 3420
 CCAGGAATGA TCTCGGTGTT AGGATTGTAA TCAAGCTCAA GCCCTCGGCG TGAAAGCTGT 3480
 AAAACCCCTT TATTTAATAC ATACCCACAG ATATCAAGAA GATTGTTACC GGGTATGGCT 3540
 TCAAGGTTTG CCTGCTTAAT TTCCTGTAAA TAACCCCATG CATAGGTAA G CATGTAATAG 3600
 ATATTACGGA CAGGTATCAC GGGCTGTTC ACTATGAGTC CCCTAATAAT TTGTTGGTCC 3660
 ATTTCTGTTG TTTATAGGGG TCATCAAAGA AATATTCTTC GAGTAAAGGG GCGATATCCG 3720
 TCATCACAAT TTCATTAAGC CATTGCGTAT CCGGAGAGGT GCCATCTTCC AACCCACAGC 3780
 AGAAGTAACT ATGCCCAATG CGGAATCCTT TCCCAAGGAT AGTGGCCTCT TTGCTGATTT 3840
 CCTGGTTCAA CTCGTTTATT TTTTGGCATA AAGACTCAAC AAATGAAGGT TCTGCTTTTT 3900
 TATTCAGTAA AAAATTCCGG AACTGTGGTG TATCAAAACC TGGCTCAATA TCTATGAAAG 3960
 AAAATCGTCT GCGTAGGGCA TAGTCAACAA CGGCCAGAGA GCGATCGGCA GTATTCATTA 4020
 AACCGATGAT ATAAACATTC TCCGCGACAT AGAATCGTTC TTCATCGTTT TCGGAGTAGG 4080
 TTAGGGGAAC AGACCAAGTT TCACCTCGTT TATCATGTTC CATTAACATC ATCACTTCGC 4140
 CAAATACTTT ACTGAGATTG GCACGATTGA TTTTATCTAT AATAAAAATA TACTTTTTCT 4200
 CTGGCTGCTC TTTAGCTTGC TGACAAAAT TGTAAATAT GCCGTCTTTA CGTCGGAAGC 4260
 CGACGCCATT CGGACGATAG CCTCTATAA AATCCTCATA GCTATAAGAT TGATGGAAT 4320
 GAACCATATT GACGCGTTGC GGAGCCTTTT CTCCTGTCAG CAAGTAAGCC AGACGGCGTG 4380
 CAACAAAGGT TTTTCCAACG CCGGGGGGCC CCTGGAGGAT AATATTTTTT TTGATGGTTA 4440
 ATCGTTTGAG TATCGTCTCT ATTGTGTTTT CAGGGATAAA CAAATCATTT AACGCATCTT 4500
 CCAGACAGTA TGATTCAGTT TTTGACATAG GTGGAATAAC ACTCTTGCCA GAATTAAATA 4560
 TTAATTTATA GTCGTTGATT ATGTTGTCCA GCATAGAGGC AAATCGGGTG TAATCAATAC 4620
 CCTGTGAGAC TTTTGGGAA CAGGCGTAAT AGGACTGTCC GTATTTTTTA GGATATACAC 4680
 CCGAAGTTGC CTGAAAATAC TCTGCGATTG TTTTAGGTAT GTCTGAAGAG AACTGCCATT 4740
 GGGCATGTGG TTCATTCTGT TCGCTTATAC CATAAGCCAA AACCAACTCA TCAAAATCTT 4800
 TATAATAGAG AATAACGGGA TATATACCGT TAGAAGCTTC CTGACCTTCT CCAAGAAATG 4860
 CAAACCAGGG AATAGACGTA AAATTACCAT AACCGAACT CAATTTTACT CGCAGGTTAC 4920
 GGTAAGACGT TGGATAATCT TTAGTGGATT GCGAACGTTG TTGCTGTGCT TGCTTAATAA 4980
 ATTTTCAAT CCAGGGTTGA ATAGATTECA TAAGATATGC CTTCTCATT GCTAAGCCTC 5040

TATTATCGCT TTCGCAACGT ACTGAAACAA TAGATTTTTTA CTGCAAAATC AGACTGGTAA 5100
ATATTTACTG AGGGGGAAAG TTTCTATTGA GTCAGTGGAA GGCTCCCGGT GGTAAACCGG 5160
GAGTAAACGC TGTTACGCGA CTTTCTGTTT ACCGGCAATC ACTCCAATAA ACGCCTGCAC 5220
CTGCTTTTGT TTACGCGCCG ACAGTTTGCA CACCTGGCGT AGCGACTGCA TCAGTTCGCT 5280
CTCCTCGGCG GCGGGTGGTT GGGCGGTGAG GACAATACAG CCTTCCATCA CTTTGACATC 5340
TACCGCCGTG CCAGTGGCAA AACCGGCGGC TTCCAGCCAC TGACCTTTCA GGGTGATGGC 5400
GGGAATACGG CTGTAATCCG GGTAGCGACT CGCATAACCG ACGGTGACAT GACGGTTATT 5460
TGCCGGGGAG ACTTCTGCTT CGAACGGTTG TGCAATAGAA TGCSTGTCAG TCATAACTGC 5520
TATTCTCCAG GAATAGTGAT TGTGATTAGC GATGCGGGTG TGTGGCGCA CATCCGCACC 5580
GCGCTAAATA CCTGTATATA TCATCAGTAA ATATGGGGAA AGTCCAGCTA AAAATAGAAT 5640
AAAATGGGCA ATTTCTGGAA TGATTTAAAT ATATTTATGT GGGTTATGAT TGGCGTGAAA 5700
TAATAAAAAG CGCACCCCAA AGGTGCGCCA GAAAATAATG TTCAGGATTT TTTACGTGAG 5760
GCTTTTTTAC CCCCCTAGC TGCGCGTTCA GCTTTGATTT TTTCCAGCAA CGCGGCGGCG 5820
CTGTTTTCTC CGCTGATCAA ATCCGGGTTT TCGGCCCCGCC ACTGGGCGGT AAGTTCACCA 5880
CGGAACGCTT TTGCCAGGAT GGATTGCGTC AGGTTGTTGA CGCGGGCTAA GGC GTTGTG 5940
ACCTGTTTTT CTATGGTGTC GCGTAGGCG AAGAGTTGCT CGACGCGGCG AACGATTTTCG 6000
GCTTGTTCTT TTA CTGGAGG TAATAAAACA ACTTGGGATT TGATATCTTT TCCTGAAATA 6060
CCTTTTTGAC CAGAAGTTGT TTTACGCAG TTCATCATTG CATTTCTGTC TGAGGGGGAT 6120
GAAAAAATA TTTCGATATA TTCTGGTAAA GCATCTTTGG TTAATCGAGC TCGAATAAGT 6180
TTATCAGGAT ATAGCAAATT TTGATGTTGT AATTTTTTCA ATAACCCACA AACACCAACA 6240
AATTCTAAAC TTCCGTTATA GCGAGTAAAT AAAAGATCTC CATCTTGTA TTTGTGGCGG 6300
TTTAGTTCAC TTTCTGAACA TTCTAGAGTC GACCTGCAGG CATGCAAGCT TGGCGTAATC 6360
ATGGTCATAG CTGTTTCCTG TGTGAAATTG TTATCCGCTC ACAATTCCAC ACAACATACG 6420
AGCCGGAAGC ATAAAGTGTA AAGCCTGGGG TGCCTAATGA GTGAGCTAAC TCACATTAAT 6480
TGCGTTGCGC TCACTGCCCC CTTTCCAGTC GGGAAACCTG TCGTGCCAGC GGATCCTCTA 6540
CGCCGGACGC ATCGTGGCCG GCATCACCGG CGCCACAGGT GCGGTTGCTG GCGCCTATAT 6600
CGCCGACATC ACCGATGGGG AAGATCGGGC TCGCCACTTC GGGCTCATGA GCGCTTGTTT 6660
CGGCGTGGGT ATGGTGGCAG GCCCCGTGGC CGGGGGACTG TTGGGCGCCA TCTCCTTGCA 6720
TGCACCATTC CTTGCGGCGG CGGTGCTCAA CGGCCTCAAC CTACTACTGG GCTGCTTCCT 6780

AATGCAGGAG	TCGCATAAGG	GAGAGCGTCG	ACCGATGCCC	TTGAGAGCCT	TCAACCCAGT	6840
CAGCTCCTTC	CGGTGGGCGC	GGGGCATGAC	TATCGTCGCC	GCACTTATGA	CTGTCTTCTT	6900
TATCATGCAA	CTCGTAGGAC	AGGTGCCGGC	AGCGCTCTGG	GTCATTTTCG	GCGAGGACCG	6960
CTTTCGCTGG	AGCGCGACGA	TGATCGGCCT	GTCGCTTGCG	GTATTGCGAA	TCTTGACACG	7020
CCTCGCTCAA	GCCTTCGTCA	CTGGTCCCGC	CACCAAACGT	TTGCGCGAGA	AGCAGGCCAT	7080
TATCGCCGGC	ATGGCGGCCG	ACGCGCTGGG	CTACGTCTTG	CTGGCGTTTC	CGACGCGAGG	7140
CTGGATGGCC	TTCCCCATTA	TGATTCTTCT	CGCTTCCGGC	GGCATCGGGA	TGCCCCGCTT	7200
GCAGGECATG	CTGTCCAGGC	AGGTAGATGA	CGACCATCAG	GGACAGCTTC	AAGGATCGCT	7260
CGCGGCTCTT	ACCAGCCTAA	CTTCGATCAT	TGGACCGCTG	ATCGTCACGG	CGATTTATGC	7320
CGCCTCGGCG	AGCACATGGA	ACGGGTGGC	ATGGATTGTA	GGCGCCGCCC	TATACCTTGT	7380
CTGCC'TCCCC	GCGTTGCGTC	GCGGTGCATG	GAGCCGGGCC	ACCTCGACCT	GAATGGAAGC	7440
CGGCGGCACC	TCGCTAACGG	ATTCACCACT	CCAAGAATTG	GAGCCAATCA	ATTCTTGCGG	7500
AGAACTGTGA	ATGCGCAAAC	CAACCCTTGG	CAGAACATAT	CCATCGCGTC	CGCCATCTCC	7560
AGCAGCCGCA	CGCGGCGCAT	CTCGGGCAGC	GTTGGGTCTT	GGCCACGGGT	GCGCATGATC	7620
GTGCTCCTGT	CGTTGAGGAC	CCGGCTAGGC	TGGCGGGGTT	GCCTTACTGG	TTAGCAGAAT	7680
GAATCACCGA	TACGCGAGCG	AACGTGAAAG	GACTGCTGCT	GCAAAACGTC	TGCGACCTGA	7740
GCAACAACAT	GAATGCTCTT	CGGTTTCCGT	GTTTCGTAAA	GTCTGGAAAC	GCGGAAGTCC	7800
CCTACGTGCT	GCTGAAGTTG	CCCGCAACAG	AGAGTGGAAC	CAACCGGTGA	TACCACGATA	7860
CTATGACTGA	GAGTCAACGC	CATGAGCGGC	CTCATTTCTT	ATTCTGAGTT	ACAACAGTCC	7920
GCACCGCTGC	CGGTAGCTCC	TTCCGGTGGG	CGCGGGGCAT	GAATATCGTC	GCCGCACTTA	7980
TGACTGTCTT	CTTTATCATG	CAACTCGTAG	GACAGGTGCC	GGCAGCGCCC	AACAGTCCCC	8040
CGGCCACGGG	GCCTGCCACC	ATACCCACGC	CGAAACAAGC	GCCCTGCACC	ATTATGTTCC	8100
GGATCTGCAT	CGCAGGATGC	TGCTGGCTAC	CCTGTGGAAC	ACCTACATCT	GTATTAAACGA	8160
AGCGCTAACC	GTTTTTATCA	GGCTCTGGGA	GGCAGAATAA	ATGATCATAT	CGTCAATTAT	8220
TACCTCCACG	GGGAGAGCCT	GAGCAAAC TG	GCCTCAGGCA	TTGAGAAGC	ACACGGTCCAC	8280
ACTGCTTCCG	GTAGTCAATA	AACCGGTAAA	CCAGCAATAG	ACATAAGCGG	CTATTTAACG	8340
ACCCTGCCCT	GAACCGACGA	CCGGGTCGAA	TTTGCTTTTC	AATTTCTGCC	ATTCATCCGC	8400
TTATTATCAC	TTATTCAAGC	GTAGCAACCA	GGCGTTTAAG	GGCACCAATA	ACTGCCTTAA	8460
AAAAATTACG	CCCCGCCCTG	CCACTCATCG	CAGTACTGTT	GTAATTCATT	AAGCATTCTG	8520

CCGACATGGA AGCCATCACA GACGGCATGA TGAACCTGAA TCGCCAGCGG CATCAGCACC 8580
 TTGTCGCCTT GCGTATAATA TTTGCCCATG GTGAAAACGG GGGCGAAGAA GTTGTCCATA 8640
 TTGGCCACGT TTAAATCAAA ACTGGTGAAA CTCACCCAGG GATTGGCTGA GACGAAAAAC 8700
 ATATTCTCAA TAAACCCTTT AGGGAAATAG GCCAGGTTTT CACCGTAACA CGCCACATCT 8760
 TGCGAATATA TGTGTAGAAA CTGCCGAAA TCGTCGTGGT ATTCACTCCA GAGCGATGAA 8820
 AACGTTTCAG TTTGCTCATG GAAAACGGTG TAACAAGGCT GAACACTATC CCATATCACC 8880
 AGCTCACCGT CTTTCATTGC CATACG 8906

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3190 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "pRM2 (target plasmid)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GCGCCCAATA CGCAAACCGC CTCTCCCCGC GCGTTGGGCG ATTCATTAAT GCAGCTGGCA 60
 CGACAGGTTT CCCGACTGGA AAGCGGGCAG TGAGCGAAG GCAATTAATG TGAGTTAGCT 120
 CACTCATTAG GCACCCACAG CTTTACACTT TATGCTTCCG GCTCGTATGT TGTGTGGAAT 180
 TGTGAGCGGA TAACAATTTT ACACAGGAAA CAGCTATGAC CATGATTACG AATTCGAGCT 240
 CGGTACCCCG GGATCCTCTA GAGTCGAGAT GCCGCATGTG GAAGAGGTGA TTGCACCGAT 300
 CTTCTACACC GTTCCGCTGC AGCTGCTGGC TTACCATGTC GCGCTGATCA AAGGCACCGA 360
 CGTTGACCAG CCGCGTAACC TGGCAAAATC GGTTACGGTT GAGTAATAAA TGGATGCCCT 420
 GCGTAAGCGG GGCATTTTTT TTCCTGTTAT GTTTTTAATC AAACATCCTG CCAACTCCAT 480
 GTGACAAACC GTCATCTTCG GCTACTTTTT CTCTGTCACA GAATGAAAAT TTTCTGTCAT 540
 CTCTTCGTTA TTAATGTTTG TAATTGACTG AATATCAACG CTTATTTAAA TCAGACTGAA 600
 GACTTATCTC TCTCTGTCAT AAAACTGTCA TATTCCTTAC ATATAACTGT CACCTGTTTG 660
 TCCTATTTTG CTTGTCGTAG CCAACAAACA ATGCTTTATG AATCCTCCCA GGAGACATTA 720
 TGAAAGTTAT GCGTACCACC GTCGCAACTG TTGTGCGCCG GACCTTATCG ACCTGCAGGC 780
 ATGCAAGCTT GGCCTGGCC GTCGTTTTAC AACGTCGTGA CTGGGAAAAC CCTGGCGTTA 840

CCCAACTTAA TCGCCTTGCA GCACATCCCC CTTTCGCCAG CTGGCGTAAT AGCGAAGAGG	900
CCCGCACCGA TCGCCCTTCC CAACAGTTGC GCAGCCTGAA TGGCGAATGG CGCCTGATGC	960
GGTATTTTCT CCTTACGCAT CTGTGCGGTA TTTCACACCG CATATGGTGC ACTCTCAGTA	1020
CAATCTGCTC TGATGCCGCA TAGTTAAGCC AGCCCCGACA CCCGCCAACA CCCGCTGACG	1080
CGCCCTGACG GGCTTGTCTG CTCCCGGCAT CCGCTTACAG ACAAGCTGTG ACCGTCTCCG	1140
GGAGCTGCAT GTGTCAGAGG TTTTCACCGT CATCACCGAA ACGCGCGAGA CGAAAGGGCC	1200
TCGTGATACG CCTATTTTTA TAGGTTAATG TCATGATAAT AATGGTTTCT TAGACGTCAG	1260
GTGGCACTTT TCGGGGAAAT GTGCGCGGAA CCCCTATTTC TTTATTTTTC TAAATACATT	1320
CAAATATGTA TCCGCTCATG AGACAATAAG CCTGATAAAT GCTTCAATAA TATTGAAAAA	1380
GGAAGAGTAT GAGTATTCAA CATTTCGGTG TCGCCCTTAT TCCCTTTTTT GCGGCATTTT	1440
GCCTTCCTGT TTTTGCTCAC CCAGAAACGC TGGTGAAAGT AAAAGATGCT GAAGATCAGT	1500
TGGGTGCACG AGTGGGTTAC ATCGAACTGG ATCTCAACAG CGGTAAGATC CTTGAGAGTT	1560
TTCGCCCCGA AGAACGTTTT CCAATGATGA GCACTTTTAA AGTTCTGCTA TGTGGCGCGG	1620
TATTATCCCG TATTGACGCC GGGCAAGAGC AACTCGGTGC CCGCATAAC TATTCTCAGA	1680
ATGACTTGGT TGAGTACTCA CCAGTCACAG AAAAGCATCT TACGGATGGC ATGACAGTAA	1740
GAGAATTATG CAGTGCTGCC ATAACCATGA GTGATAACAC TCGCGCAAAC TTAATTCTGA	1800
CAACGATCGG AGGACCGAAG GAGCTAACCG CTTTTTTGCA CAACATGGGG GATCATGTAA	1860
CTCGCCTTGA TCGTTGGGAA CCGGAGCTGA ATGAAGCCAT ACCAAACGAC GAGGCTGACA	1920
CCACGATGCC TGTAGCAATG GCAACAACGT TGCGCAAAC ATTAAGTGGC GAACTACTTA	1980
CTCTAGCTTC CCGGCAACAA TTAATAGACT GGATGGAGGC GGATAAAGTT GCAGGACCAC	2040
TTCTGCGCTC GGCCCTTCCG GCTGGCTGCT TTATTGCTGA TAAATCTGGA GCCGCTGAGC	2100
GTGGGTCTCG CGGTATCATT GCAGCACTGG GGCCAGATGG TAAGCCCTCC CGTATCGTAG	2160
TTATCTACAC GACGGGGAGT CAGGCAACTA TGGATGAACG AAATAGACAG ATCGCTGAGA	2220
TAGGTGCCTC ACTGATTAAG CATTGGTAAC TGTCAGACCA AGTTTACTCA TATATACTTT	2280
AGATTGATTT AAAACTTCAT TTTTAATTTA AAAGGATCTA GGTGAAGATC CTTTTTGATA	2340
ATCTCATGAC CAAAATCCCT TAACGTGAGT TTTCGTTCCA CTGAGCGTCA GACCCCGTAG	2400
AAAAGATCAA AGGATCTTCT TGAGATCCTT TTTTCTGCG CGTAATCTGC TGCTTGCAAA	2460
CAAAAAAACC ACCGCTACCA GCGGTGGTTT GTTTGCCGGA TCAAGAGCTA CCAACTCTTT	2520
TTCCGAAGGT AACTGGCTTC AGCAGAGCGC AGATACCAAA TACTGTCCTT CTAGTGTAGC	2580

CGTAGTTAGG CCACCACTTC AAGAACTCTG TAGCACCGCC TACATACCTC GCTCTGCTAA	2640
TCCTGTTACC AGTGGCTGCT GCCAGTGGCG ATAAGTCGTG TCTTACCGGG TTGGA CTCAA	2700
GACGATAGTT ACCGGATAAG GCGCAGCGGT CGGGCTGAAC GGGGGGTTTCG TGCACACAGC	2760
CCAGCTTGGA GCGAACGACC TACACCGAAC TGAGATACCT ACAGCGTGAG CTATGAGAAA	2820
GCGCCACGCT TCCCGAAGGG AGAAAGGCGG ACAGGTATCC GGTAAGCGGC AGGGTCGGAA	2880
CAGGAGAGCG CACGAGGGAG CTTCCAGGGG GAAACGCCTG GTATCTTTAT AGTCCTGTCTG	2940
GGTTTCGCCA CCTCTGACTT GAGCGTCGAT TTTTGTGATG CTCGTCAGGG GGGCGGAGCC	3000
TATGGAAAAA CGCCAGCAAC GCGGCCTTTT TACGGTTCCF GGCCTTTTGC TGGCCTTTTG	3060
CTCACATGTT CTTCCTGCG TTATCCCGTG ATTCTGTGGA TAACCGTATT ACCGCCTTTG	3120
AGTGAGCTGA TACCGCTCGC CGCAGCCGAA CGACCGAGCG CAGCGAGTCA GTGAGCGAGG	3180
AAGCGGAAGA	3190

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Oligonucleotide (NLC95)
used to analyze products of transposition."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATAATCCTTA AAAACTCCAT TTCCACCCCT

30

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Oligonucleotide (NLC209)
used to analyze products of transposition"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTGATTGCAC CGATCTTCTA CACCGTTCC

29

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide (NLC429)
used to analyze products of transposition"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTTCACCGTC ATCACCGAAA CGCGCGAGAC

30

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide (NLC430)
used to analyze products of transposition"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AATGACTTGG TTGAGTACTC ACCAGTCACA

30

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide (NLC431)
used to analyze the products of transposition"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGAACGAAA TAGACAGATC GCTGAGATAG

30

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligonucleotide (NLC432)
 used to analyze products of transposition"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CAAGACGATA GTTACCGGAT AAGGCGCAGC

30

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligonucleotide (NLC94)
 used for sequence determination"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AAAGTCCAGT ATGCTTTTTC ACAGCATAAC

30

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Asn Tyr Asn Arg Asn
1 5

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Asn	Tyr	Thr	Arg	Asn
1				5